

SEQUENCE LISTING

<110> Peoples, Oliver P
 Madison, Lara L
 Huisman, Gjalt W

<120> Enzymes for Biopolymer Production

<130> MBX 030

<140> unknown

<141> 1999-07-30

<150> 60/094,674

<151> 1998-07-30

<160> 61

<170> PatentIn Ver. 2.0

<210> 1

<211> 1182

<212> DNA

<213> *Alcaligenes eutrophus*

<220>

<221> gene

<222> (1)..(1182)

<223> *phbA* gene

<400> 1

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650E20" 24349E60

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<210> 2
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 <212> PRT
 <213> *Alcaligenes eutrophus*

<220>
 <221> PEPTIDE
 <222> (1)..(393)
 <223> beta-ketothiolase

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 Phe Gly Gly Ser Leu Ala Lys Ile Pro Ala Pro Glu Leu Gly Ala Val
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 35 40 45
 Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser Gly Gln Asn
 50 55 60
 Pro Ala Arg Gln Ala Ala Ile Lys Ala Gly Leu Pro Ala Met Val Pro
 65 70 75 80
 Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys Ala Val Met
 85 90 95
 Leu Ala Ala Asn Ala Ile Met Ala Gly Asp Ala Glu Ile Val Val Ala
 100 105 110
 Gly Gly Gln Glu Asn Met Ser Ala Ala Pro His Val Leu Pro Gly Ser
 115 120 125
 Arg Asp Gly Phe Arg Met Gly Asp Ala Lys Leu Val Asp Thr Met Ile
 130 135 140
 Val Asp Gly Leu Trp Asp Val Tyr Asn Gln Tyr His Met Gly Ile Thr
 145 150 155 160
 Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu Ala Gln Asp
 165 170 175

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Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala Gln Lys Ala
 180 185 190

Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro Gln Arg Lys
 195 200 205

Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg Gln Gly Ala
 210 215 220

Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp Lys Ala Gly
 225 230 235 240

Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly Ala Ala Ala
 245 250 255

Val Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly Leu Thr Pro
 260 265 270

Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp Pro Lys Val
 275 280 285

Met Gly Met Gly Pro Val Pro Ala Ser Lys Arg Ala Leu Ser Arg Ala
 290 295 300

Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn Glu Ala Phe
 305 310 315 320

Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp Asp Thr Ser
 325 330 335

Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His Pro Ile Gly
 340 345 350

Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu Met Lys Arg
 355 360 365

Arg Asp Ala Lys Lys Gly Leu Ala Ser Leu Cys Ile Gly Gly Gly Met
 370 375 380

Gly Val Ala Leu Ala Val Glu Arg Lys
 385 390

<210> 3

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

oligonucleotide primer- AlFKpn

<400> 3

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43

<210> 4

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

oligonucleotide primer- AlF-Bam

<400> 4

cgcggtatcct ttgcgctcga ctgccagcgc caccgccc

37

<210> 5

<211> 741

<212> DNA

<213> *Alcaligenes eutrophus*

<220>

<221> gene

<222> (1)..(741)

<223> phbB gene

<400> 5

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cgcgaaaagt ggctggagca gcagaaggcc ctgggcttcg atttcattgc ctcggaaggc 180
aatgtggctg actgggactc gaccaagacc gcattcgaca aggtcaagtc cgaggtcggc 240
gaggttgatg tgctgatcaa caacgccggc atcaccgcgc acgtggtgtt ccgcaagatg 300
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aagcaggtga tcgacggcat ggccgaccgt ggctggggcc gcacgtcaa catctcgtcg 420
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aagatcgctc cgacgatccc ggtcaagcgc ctgggcctgc cggaagagat cgcctcgatc 660
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ggcggcctgc atatgggctg a 741

<210> 6

<211> 246

<212> PRT

<213> *Alcaligenes eutrophus*

<220>

<221> PEPTIDE

<222> (1)..(246)

<223> reductase

<400> 6

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Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
35 40 45

Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
50 55 60

Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
65 70 75 80

Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val
85 90 95

Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn
100 105 110

Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
115 120 125

Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
130 135 140

Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
145 150 155 160

His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
165 170 175

Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys
180 185 190

Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val
195 200 205

Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu
210 215 220

550E20" 24349E60

Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn
 225 230 235 240

Gly Gly Leu His Met Gly
 245

<210> 7
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide primer-B1L-Bam

<400> 7
 cgcggatcca tgactcagcg cattgcgtat gtgacc 36

<210> 8
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide primer- B1L-Xba

<400> 8
 gctctagatc agcccatatg caggccgccg ttgagcg 37

<210> 9
 <211> 1926
 <212> DNA
 <213> Alcaligenes eutrophus

<220>
 <221> misc_feature
 <222> (1)..(1926)
 <223> phbA-linker-phbB fusion gene

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 gccggcgtca agccggagca ggtgagcgaa gtcacatcgt gccaggtgct gaccgccggt 180
 tcggggccaga accccgcacg ccaggccgcg atcaaggccg gcctgccggc gatggtgccg 240
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gacaccatga tcgtcgacgg cctgtgggac gtgtacaacc agtaccacat gggcatcacc 480
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ggctga 1926
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<210> 10

<211> 641

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thredase
Fusion Protein

<220>

<221> PEPTIDE

<222> (1)..(641)

<400> 10

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    20             25             30
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Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val Lys Pro Glu Gln Val
 35 40 45
 Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser Gly Gln Asn
 50 55 60
 Pro Ala Arg Gln Ala Ala Ile Lys Ala Gly Leu Pro Ala Met Val Pro
 65 70 75 80
 Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys Ala Val Met
 85 90 95
 Leu Ala Ala Asn Ala Ile Met Ala Gly Asp Ala Glu Ile Val Val Ala
 100 105 110
 Gly Gly Gln Glu Asn Met Ser Ala Ala Pro His Val Leu Pro Gly Ser
 115 120 125
 Arg Asp Gly Phe Arg Met Gly Asp Ala Lys Leu Val Asp Thr Met Ile
 130 135 140
 Val Asp Gly Leu Trp Asp Val Tyr Asn Gln Tyr His Met Gly Ile Thr
 145 150 155 160
 Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu Ala Gln Asp
 165 170 175
 Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala Gln Lys Ala
 180 185 190
 Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro Gln Arg Lys
 195 200 205
 Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg Gln Gly Ala
 210 215 220
 Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp Lys Ala Gly
 225 230 235 240
 Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly Ala Ala Ala
 245 250 255
 Val Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly Leu Thr Pro
 260 265 270
 Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp Pro Lys Val
 275 280 285

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Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp Asp Thr Ser	325	330	335
Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His Pro Ile Gly	340	345	350
Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu Met Lys Arg	355	360	365
Arg Asp Ala Lys Lys Gly Leu Ala Ser Leu Cys Ile Gly Gly Gly Met	370	375	380
Gly Val Ala Leu Ala Val Glu Arg Lys Gly Ser Met Thr Gln Arg Ile	385	390	395 400
Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly Thr Ala Ile Cys Gln	405	410	415
Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala Gly Cys Gly Pro Asn	420	425	430
Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln Lys Ala Leu Gly Phe	435	440	445
Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp Trp Asp Ser Thr Lys	450	455	460
Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly Glu Val Asp Val Leu	465	470	475 480
Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val Phe Arg Lys Met Thr	485	490	495
Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn Leu Thr Ser Leu Phe	500	505	510
Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala Asp Arg Gly Trp Gly	515	520	525
Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln Lys Gly Gln Phe Gly	530	535	540

Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu His Gly Phe Thr Met
545 550 555 560

Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val Thr Val Asn Thr Val
565 570 575

Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys Ala Ile Arg Gln Asp
580 585 590

Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val Lys Arg Leu Gly Leu
595 600 605

Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu Ser Ser Glu Glu Ser
610 615 620

Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn Gly Gly Leu His Met
625 630 635 640

Gly

<210> 11

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
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<400> 11

gatctaccg

9

<210> 12

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide primer- L5B

<400> 12

atggcctag

9

<210> 13

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide Linker

<220>
<221> PEPTIDE
<222> (1)..(5)

<400> 13
Gly Ser Thr Gly Ser
1 5

<210> 14
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer- B1F-Kpn

<400> 14
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46

<210> 15
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer- B1F-BamHI

<400> 15
cgcggatccg cccatatgca ggccgccggtt gagcg

35

<210> 16
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer- A1L BamHI

<400> 16
cgcggtatcca tgactgacgt tgtcatcgta tcc 33

<210> 17
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer- All-XbaI

<400> 17
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<210> 18
<211> 1926
<212> DNA
<213> Artificial Sequence

<220>
<221> gene
<222> (1)..(1926)
<223> phbB-linker-phbA fusion gene

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gcgtcgggct gccgtatcct ggtgacgctg ctgcacgaga tgaagcgccg tgacgcgaag 1860
aagggcctgg cctcgctgtg catcggcggc ggcattggcg tggcgctggc agtcgagcgc 1920
aaataa 1926

<210> 19

<211> 641

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reductase
Fusion Protein

<220>

<221> PEPTIDE

<222> (1)..(641)

<400> 19

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			20					25					30		
Gly	Cys	Gly	Pro	Asn	Ser	Pro	Arg	Arg	Glu	Lys	Trp	Leu	Glu	Gln	Gln
		35					40					45			
Lys	Ala	Leu	Gly	Phe	Asp	Phe	Ile	Ala	Ser	Glu	Gly	Asn	Val	Ala	Asp
	50					55					60				
Trp	Asp	Ser	Thr	Lys	Thr	Ala	Phe	Asp	Lys	Val	Lys	Ser	Glu	Val	Gly
65				70					75					80	
Glu	Val	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Val	Val
			85					90					95		
Phe	Arg	Lys	Met	Thr	Arg	Ala	Asp	Trp	Asp	Ala	Val	Ile	Asp	Thr	Asn
		100						105					110		

Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
115 120 125

Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
130 135 140

Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
145 150 155 160

His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
165 170 175

Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys
180 185 190

Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val
195 200 205

Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu
210 215 220

Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn
225 230 235 240

Gly Gly Leu His Met Gly Gly Ser Met Thr Asp Val Val Ile Val Ser
245 250 255

Ala Ala Arg Thr Ala Val Gly Lys Phe Gly Gly Ser Leu Ala Lys Ile
260 265 270

Pro Ala Pro Glu Leu Gly Ala Val Val Ile Lys Ala Ala Leu Glu Arg
275 280 285

Ala Gly Val Lys Pro Glu Gln Val Ser Glu Val Ile Met Gly Gln Val
290 295 300

Leu Thr Ala Gly Ser Gly Gln Asn Pro Ala Arg Gln Ala Ala Ile Lys
305 310 315 320

Ala Gly Leu Pro Ala Met Val Pro Ala Met Thr Ile Asn Lys Val Cys
325 330 335

Gly Ser Gly Leu Lys Ala Val Met Leu Ala Ala Asn Ala Ile Met Ala
340 345 350

Gly Asp Ala Glu Ile Val Val Ala Gly Gly Gln Glu Asn Met Ser Ala
355 360 365

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Ala Pro His Val Leu Pro Gly Ser Arg Asp Gly Phe Arg Met Gly Asp
 370 375 380
 Ala Lys Leu Val Asp Thr Met Ile Val Asp Gly Leu Trp Asp Val Tyr
 385 390 395 400
 Asn Gln Tyr His Met Gly Ile Thr Ala Glu Asn Val Ala Lys Glu Tyr
 405 410 415
 Gly Ile Thr Arg Glu Ala Gln Asp Glu Phe Ala Val Gly Ser Gln Asn
 420 425 430
 Lys Ala Glu Ala Ala Gln Lys Ala Gly Lys Phe Asp Glu Glu Ile Val
 435 440 445
 Pro Val Leu Ile Pro Gln Arg Lys Gly Asp Pro Val Ala Phe Lys Thr
 450 455 460
 Asp Glu Phe Val Arg Gln Gly Ala Thr Leu Asp Ser Met Ser Gly Leu
 465 470 475 480
 Lys Pro Ala Phe Asp Lys Ala Gly Thr Val Thr Ala Ala Asn Ala Ser
 485 490 495
 Gly Leu Asn Asp Gly Ala Ala Ala Val Val Val Met Ser Ala Ala Lys
 500 505 510
 Ala Lys Glu Leu Gly Leu Thr Pro Leu Ala Thr Ile Lys Ser Tyr Ala
 515 520 525
 Asn Ala Gly Val Asp Pro Lys Val Met Gly Met Gly Pro Val Pro Ala
 530 535 540
 Ser Lys Arg Ala Leu Ser Arg Ala Glu Trp Thr Pro Gln Asp Leu Asp
 545 550 555 560
 Leu Met Glu Ile Asn Glu Ala Phe Ala Ala Gln Ala Leu Ala Val His
 565 570 575
 Gln Gln Met Gly Trp Asp Thr Ser Lys Val Asn Val Asn Gly Gly Ala
 580 585 590
 Ile Ala Ile Gly His Pro Ile Gly Ala Ser Gly Cys Arg Ile Leu Val
 595 600 605
 Thr Leu Leu His Glu Met Lys Arg Arg Asp Ala Lys Lys Gly Leu Ala
 610 615 620

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Ser Leu Cys Ile Gly Gly Gly Met Gly Val Ala Leu Ala Val Glu Arg
625 630 635 640

Lys

<210> 20
<211> 1680
<212> DNA
<213> *Pseudomonas oleovorans*

<220>
<221> gene
<222> (1)..(1680)
<223> phbC1 gene

<400> 20
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caggccgtgc gcccaaccgct gcacagcgcc aagcatgtgg ccacttttg cctggagctg 180
aagaacgtgc tgctgggcaa gtccagcctt gccccgaaa gcgacgaccg tcgcttcaat 240
gaccggtcat ggagcaacaa ccactttac cgccgctacc tgcaaaccta tctggcctgg 300
cgcaaggagc tgcaggactg gatcggcaac agcgacctgt cggcccagga catcagccgc 360
ggccagtctg tcatcaacct gatgaccgaa gccatggctc cgaccaacac cctgtccaac 420
ccggcagcag tcaaacgctt cttcgaaacc ggccggcaaga gcctgctcga tggcctgtcc 480
aacctggcca aggacctggt caacaacggt ggcattgcca gccaggtgaa catggacgcc 540
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cactggcaaa gctggctggg cgagcgtgcc ggccgagctgg aaaaggcgcc gaccgcctg 1620
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<210> 21

<211> 559
 <212> PRT
 <213> Pseudomonas oleovorans

<220>
 <221> PEPTIDE
 <222> (1)..(559)
 <223> PHA Polymerase

<400> 21

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      20              25              30

Ser Ser Ala Arg Thr Val Leu Arg Gln Ala Val Arg Gln Pro Leu His
      35              40              45

Ser Ala Lys His Val Ala His Phe Gly Leu Glu Leu Lys Asn Val Leu
      50              55              60

Leu Gly Lys Ser Ser Leu Ala Pro Glu Ser Asp Asp Arg Arg Phe Asn
      65              70              75              80

Asp Pro Ala Trp Ser Asn Asn Pro Leu Tyr Arg Arg Tyr Leu Gln Thr
      85              90              95

Tyr Leu Ala Trp Arg Lys Glu Leu Gln Asp Trp Ile Gly Asn Ser Asp
      100             105             110

Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Met
      115             120             125

Thr Glu Ala Met Ala Pro Thr Asn Thr Leu Ser Asn Pro Ala Ala Val
      130             135             140

Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Ser
      145             150             155             160

Asn Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val
      165             170             175

Asn Met Asp Ala Phe Glu Val Gly Lys Asn Leu Gly Thr Ser Glu Gly
      180             185             190

Ala Val Val Tyr Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Lys Pro
      195             200             205
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09364960 2134960

660620 2494950

Ile Thr Glu Gln Val His Ala Arg Pro Leu Leu Val Val Pro Pro Gln		
210	215	220
Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Glu Lys Ser Leu Ala		
225	230	235 240
Arg Tyr Cys Leu Arg Ser Gln Gln Gln Thr Phe Ile Ile Ser Trp Arg		
	245	250 255
Asn Pro Thr Lys Ala Gln Arg Glu Trp Gly Leu Ser Thr Tyr Ile Asp		
	260	265 270
Ala Leu Lys Glu Ala Val Asp Ala Val Leu Ala Ile Thr Gly Ser Lys		
	275	280 285
Asp Leu Asn Met Leu Gly Ala Cys Ser Gly Gly Ile Thr Cys Thr Ala		
	290	295 300
Leu Val Gly His Tyr Ala Ala Leu Gly Glu Asn Lys Val Asn Ala Leu		
305	310	315 320
Thr Leu Leu Val Ser Val Leu Asp Thr Thr Met Asp Asn Gln Val Ala		
	325	330 335
Leu Phe Val Asp Glu Gln Thr Leu Glu Ala Ala Lys Arg His Ser Tyr		
	340	345 350
Gln Ala Gly Val Leu Glu Gly Ser Glu Met Ala Lys Val Phe Ala Trp		
	355	360 365
Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu		
	370	375 380
Leu Gly Asn Glu Pro Pro Val Phe Asp Ile Leu Phe Trp Asn Asn Asp		
385	390	395 400
Thr Thr Arg Leu Pro Ala Ala Phe His Gly Asp Leu Ile Glu Met Phe		
	405	410 415
Lys Ser Asn Pro Leu Thr Arg Pro Asp Ala Leu Glu Val Cys Gly Thr		
	420	425 430
Pro Ile Asp Leu Lys Gln Val Lys Cys Asp Ile Tyr Ser Leu Ala Gly		
	435	440 445
Thr Asn Asp His Ile Thr Pro Trp Gln Ser Cys Tyr Arg Ser Ala His		
450	455	460

Leu Phe Gly Gly Lys Ile Glu Phe Val Leu Ser Asn Ser Gly His Ile
465 470 475 480

Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr
485 490 495

Gly Ala Asp Arg Pro Gly Asp Pro Val Ala Trp Gln Glu Asn Ala Thr
500 505 510

Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Ser Trp Leu Gly Glu
515 520 525

Arg Ala Gly Glu Leu Glu Lys Ala Pro Thr Arg Leu Gly Asn Arg Ala
530 535 540

Tyr Ala Ala Gly Glu Ala Ser Pro Gly Thr Tyr Val His Glu Arg
545 550 555

<210> 22

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide primer- C3 up I

<400> 22

ggaattcagg aggttttatg agtaacaaga acaacgatga gc

42

<210> 23

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide primer- C3 up II

<400> 23

cgggatccac gctcgtgaac gtaggtgccc

30

<210> 24

<211> 30

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide primer- C3 dw I

<400> 24
 cgggatccag taacaagaac aacgatgagc 30

<210> 25
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide primer- C3 dw II

<400> 25
 gctctagaag ctttcaacgc tcgtgaacgt aggtgccc 38

<210> 26
 <211> 888
 <212> DNA
 <213> Pseudomonas putida

<220>
 <221> gene
 <222> (1) .. (888)
 <223> phaG

<400> 26
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 gcctcgttcg cccagacggt acgtaacctg caccacagat tcaacgtggt tctgttcgac 180
 cagccgtatt caggcaagtc caagccgcac aaccgtcagg aacggctgat cagcaaggag 240
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 ttttcgtggg gtggcgcaag cacgctgctg gcgctggcgc accagccgcg gtacgtgaag 360
 aaggcagtgg tgagtctggt ctgcgccagt atcaacgagc cgatgcgcga ctatctggac 420
 cgtggctgcc agtacctggc cgcctgcgac cgttatcagg tcggcaacct ggtcaatgac 480
 accatcgcca agcacttgcc gtcgctgttc aaacgcttca actaccgcca tgtgagcagc 540
 ctggacagcc acgagtacgc acagatgcac ttccacatca accaggtgct ggagcacgac 600
 ctggaacgtg cgctgcaagg cgcgcgcaat atcaacatcc cgggtgctgtt catcaacggc 660
 gagcgcgacg agtacaccac agtcgaggat gcgcggcagt tcagcaagca tgtgggcaga 720
 agccagttca gcgtgatccg cgatgcgggc cacttcctgg acatggagaa caagaccgcc 780
 tgcgagaaca cccgcaatgt catgctgggc ttcctcaagc caaccgtgcg tgaaccccg 840
 caacgttacc aaccctgca gcaggggcag catgcatttg ccatctga 888

<210> 27

<211> 295
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: acyl ACP-CoA
 transferase

<220>

<221> PEPTIDE

<222> (1)..(295)

<400> 27

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Met Arg Pro Glu Ile Ala Val Leu Asp Ile Gln Gly Gln Tyr Arg Val
  1             5             10             15

Tyr Thr Glu Phe Tyr Arg Ala Asp Ala Ala Glu Asn Thr Ile Ile Leu
      20             25             30

Ile Asn Gly Ser Leu Ala Thr Thr Ala Ser Phe Ala Gln Thr Val Arg
      35             40             45

Asn Leu His Pro Gln Phe Asn Val Val Leu Phe Asp Gln Pro Tyr Ser
      50             55             60

Gly Lys Ser Lys Pro His Asn Arg Gln Glu Arg Leu Ile Ser Lys Glu
      65             70             75             80

Thr Glu Ala His Ile Leu Leu Glu Leu Ile Glu His Phe Gln Ala Asp
      85             90             95

His Val Met Ser Phe Ser Trp Gly Gly Ala Ser Thr Leu Leu Ala Leu
      100            105            110

Ala His Gln Pro Arg Tyr Val Lys Lys Ala Val Val Ser Ser Phe Ser
      115            120            125

Pro Val Ile Asn Glu Pro Met Arg Asp Tyr Leu Asp Arg Gly Cys Gln
      130            135            140

Tyr Leu Ala Ala Cys Asp Arg Tyr Gln Val Gly Asn Leu Val Asn Asp
      145            150            155            160

Thr Ile Gly Lys His Leu Pro Ser Leu Phe Lys Arg Phe Asn Tyr Arg
      165            170            175

His Val Ser Ser Leu Asp Ser His Glu Tyr Ala Gln Met His Phe His
      180            185            190

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Ile Asn Gln Val Leu Glu His Asp Leu Glu Arg Ala Leu Gln Gly Ala
 195 200 205

Arg Asn Ile Asn Ile Pro Val Leu Phe Ile Asn Gly Glu Arg Asp Glu
 210 215 220

Tyr Thr Thr Val Glu Asp Ala Arg Gln Phe Ser Lys His Val Gly Arg
 225 230 235 240

Ser Gln Phe Ser Val Ile Arg Asp Ala Gly His Phe Leu Asp Met Glu
 245 250 255

Asn Lys Thr Ala Cys Glu Asn Thr Arg Asn Val Met Leu Gly Phe Leu
 260 265 270

Lys Pro Thr Val Arg Glu Pro Arg Gln Arg Tyr Gln Pro Val Gln Gln
 275 280 285

Gly Gln His Ala Phe Ala Ile
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<210> 28

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 oligonucleotide primer- G3 dw I

<400> 28

cgggatccag gccagaaatc gctgtacttg

30

<210> 29

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 oligonucleotide primer- G3 dw II

<400> 29

gctctagaag ctttcagatg gcaaatgcat gctgcccc

38

<210> 30

<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer- G3 up I

<400> 30
ggaattcagg aggttttatg aggccagaaa tcgctgtact tg 42

<210> 31
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer- G3 up II

<400> 31
cgggatccga tggcaaatgc atgctgcccc 30

<210> 32
<211> 2571
<212> DNA
<213> Pseudomonas putida

<220>
<221> gene
<222> (1)..(2571)
<223> phaC1-linker-phaG fusion gene

<400> 32
atgagtaaca agaacaacga tgagctgcag cggcaggcct cggaaaacac cctggggctg 60
aaccgggtca tcggtatccg ccgcaaagac ctgttgagct cggcacgcac cgtgctgcgc 120
caggccgtgc gccaacccgt gcacagcgcc aagcatgtgg ccacttttg cctggagctg 180
aagaacgtgc tgctgggcaa gtccagcctt gccccggaaa gcgacgaccg tcgcttcaat 240
gacccggcat ggagcaacaa ccacttttac cgccgctacc tgcaaacctt tctggcctgg 300
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gcccagcgcg aatggggcct gtccacctac atcgacgcgc tcaaggaggc ggtcgacgcg 840

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gcctgcgaga acacccgcaa tgtcatgctg ggcttctcctca agccaaccgt gcgtgaaccc 2520
cgccaacgtt accaaccctg gcagcagggg cagcatgcat ttgccatctg a 2571

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<210> 33

<211> 856

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthase Acyl
ACP-CoA Transferase Fusion Protein

<220>

<221> PEPTIDE

<222> (1)..(856)

<400> 33

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1

5

10

15

Thr Leu Gly Leu Asn Pro Val Ile Gly Ile Arg Arg Lys Asp Leu Leu

660E2D-24849E6D

20	25	30	
Ser Ser Ala Arg Thr Val Leu Arg Gln Ala Val Arg Gln Pro Leu His			
35	40	45	
Ser Ala Lys His Val Ala His Phe Gly Leu Glu Leu Lys Asn Val Leu			
50	55	60	
Leu Gly Lys Ser Ser Leu Ala Pro Glu Ser Asp Asp Arg Arg Phe Asn			
65	70	75	80
Asp Pro Ala Trp Ser Asn Asn Pro Leu Tyr Arg Arg Tyr Leu Gln Thr			
85	90	95	
Tyr Leu Ala Trp Arg Lys Glu Leu Gln Asp Trp Ile Gly Asn Ser Asp			
100	105	110	
Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Met			
115	120	125	
Thr Glu Ala Met Ala Pro Thr Asn Thr Leu Ser Asn Pro Ala Ala Val			
130	135	140	
Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Ser			
145	150	155	160
Asn Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val			
165	170	175	
Asn Met Asp Ala Phe Glu Val Gly Lys Asn Leu Gly Thr Ser Glu Gly			
180	185	190	
Ala Val Val Tyr Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Lys Pro			
195	200	205	
Ile Thr Glu Gln Val His Ala Arg Pro Leu Leu Val Val Pro Pro Gln			
210	215	220	
Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Glu Lys Ser Leu Ala			
225	230	235	240
Arg Tyr Cys Leu Arg Ser Gln Gln Gln Thr Phe Ile Ile Ser Trp Arg			
245	250	255	
Asn Pro Thr Lys Ala Gln Arg Glu Trp Gly Leu Ser Thr Tyr Ile Asp			
260	265	270	
Ala Leu Lys Glu Ala Val Asp Ala Val Leu Ala Ile Thr Gly Ser Lys			

650E20" 24849E60

275		280		285
Asp Leu Asn Met Leu Gly Ala Cys Ser Gly Gly Ile Thr Cys Thr Ala				
290		295		300
Leu Val Gly His Tyr Ala Ala Leu Gly Glu Asn Lys Val Asn Ala Leu				
305		310		315
Thr Leu Leu Val Ser Val Leu Asp Thr Thr Met Asp Asn Gln Val Ala				
	325		330	335
Leu Phe Val Asp Glu Gln Thr Leu Glu Ala Ala Lys Arg His Ser Tyr				
	340		345	350
Gln Ala Gly Val Leu Glu Gly Ser Glu Met Ala Lys Val Phe Ala Trp				
	355		360	365
Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu				
	370		375	380
Leu Gly Asn Glu Pro Pro Val Phe Asp Ile Leu Phe Trp Asn Asn Asp				
	385		390	395
Thr Thr Arg Leu Pro Ala Ala Phe His Gly Asp Leu Ile Glu Met Phe				
	405		410	415
Lys Ser Asn Pro Leu Thr Arg Pro Asp Ala Leu Glu Val Cys Gly Thr				
	420		425	430
Pro Ile Asp Leu Lys Gln Val Lys Cys Asp Ile Tyr Ser Leu Ala Gly				
	435		440	445
Thr Asn Asp His Ile Thr Pro Trp Gln Ser Cys Tyr Arg Ser Ala His				
	450		455	460
Leu Phe Gly Gly Lys Ile Glu Phe Val Leu Ser Asn Ser Gly His Ile				
	465		470	475
Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr				
	485		490	495
Gly Ala Asp Arg Pro Gly Asp Pro Val Ala Trp Gln Glu Asn Ala Thr				
	500		505	510
Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Ser Trp Leu Gly Glu				
	515		520	525
Arg Ala Gly Glu Leu Glu Lys Ala Pro Thr Arg Leu Gly Asn Arg Ala				

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530		535		540	
Tyr Ala Ala Gly Glu Ala Ser Pro Gly Thr Tyr Val His Glu Arg Gly					
545		550		555	560
Phe Met Arg Pro Glu Ile Ala Val Leu Asp Ile Gln Gly Gln Tyr Arg					
	565		570		575
Val Tyr Thr Glu Phe Tyr Arg Ala Asp Ala Ala Glu Asn Thr Ile Ile					
	580		585		590
Leu Ile Asn Gly Ser Leu Ala Thr Thr Ala Ser Phe Ala Gln Thr Val					
	595		600		605
Arg Asn Leu His Pro Gln Phe Asn Val Val Leu Phe Asp Gln Pro Tyr					
	610		615		620
Ser Gly Lys Ser Lys Pro His Asn Arg Gln Glu Arg Leu Ile Ser Lys					
	625		630		635
Glu Thr Glu Ala His Ile Leu Leu Glu Leu Ile Glu His Phe Gln Ala					
		645		650	655
Asp His Val Met Ser Phe Ser Trp Gly Gly Ala Ser Thr Leu Leu Ala					
	660		665		670
Leu Ala His Gln Pro Arg Tyr Val Lys Lys Ala Val Val Ser Ser Phe					
	675		680		685
Ser Pro Val Ile Asn Glu Pro Met Arg Asp Tyr Leu Asp Arg Gly Cys					
	690		695		700
Gln Tyr Leu Ala Ala Cys Asp Arg Tyr Gln Val Gly Asn Leu Val Asn					
	705		710		715
Asp Thr Ile Gly Lys His Leu Pro Ser Leu Phe Lys Arg Phe Asn Tyr					
	725		730		735
Arg His Val Ser Ser Leu Asp Ser His Glu Tyr Ala Gln Met His Phe					
	740		745		750
His Ile Asn Gln Val Leu Glu His Asp Leu Glu Arg Ala Leu Gln Gly					
	755		760		765
Ala Arg Asn Ile Asn Ile Pro Val Leu Phe Ile Asn Gly Glu Arg Asp					
	770		775		780
Glu Tyr Thr Thr Val Glu Asp Ala Arg Gln Phe Ser Lys His Val Gly					


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gtcaaacgct tcttcgaaac cggcggcaag agcctgctcg atggcctgtc caacctggcc 1380
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<210> 35

<211> 856

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Acyl ACP-CoA
Transferase Synthase Fusion Protein

<220>

<221> PEPTIDE

<222> (1)..(856)

<400> 35

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Met Arg Pro Glu Ile Ala Val Leu Asp Ile Gln Gly Gln Tyr Arg Val
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```

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Tyr Thr Glu Phe Tyr Arg Ala Asp Ala Ala Glu Asn Thr Ile Ile Leu
      20             25             30

```

```

Ile Asn Gly Ser Leu Ala Thr Thr Ala Ser Phe Ala Gln Thr Val Arg
    35             40             45

```

```

Asn Leu His Pro Gln Phe Asn Val Val Leu Phe Asp Gln Pro Tyr Ser
    50             55             60

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660E20" 2484847" 073099

Gly	Lys	Ser	Lys	Pro	His	Asn	Arg	Gln	Glu	Arg	Leu	Ile	Ser	Lys	Glu	65	70	75	80
Thr	Glu	Ala	His	Ile	Leu	Leu	Glu	Leu	Ile	Glu	His	Phe	Gln	Ala	Asp	85	90	95	
His	Val	Met	Ser	Phe	Ser	Trp	Gly	Gly	Ala	Ser	Thr	Leu	Leu	Ala	Leu	100	105	110	
Ala	His	Gln	Pro	Arg	Tyr	Val	Lys	Lys	Ala	Val	Val	Ser	Ser	Phe	Ser	115	120	125	
Pro	Val	Ile	Asn	Glu	Pro	Met	Arg	Asp	Tyr	Leu	Asp	Arg	Gly	Cys	Gln	130	135	140	
Tyr	Leu	Ala	Ala	Cys	Asp	Arg	Tyr	Gln	Val	Gly	Asn	Leu	Val	Asn	Asp	145	150	155	160
Thr	Ile	Gly	Lys	His	Leu	Pro	Ser	Leu	Phe	Lys	Arg	Phe	Asn	Tyr	Arg	165	170	175	
His	Val	Ser	Ser	Leu	Asp	Ser	His	Glu	Tyr	Ala	Gln	Met	His	Phe	His	180	185	190	
Ile	Asn	Gln	Val	Leu	Glu	His	Asp	Leu	Glu	Arg	Ala	Leu	Gln	Gly	Ala	195	200	205	
Arg	Asn	Ile	Asn	Ile	Pro	Val	Leu	Phe	Ile	Asn	Gly	Glu	Arg	Asp	Glu	210	215	220	
Tyr	Thr	Thr	Val	Glu	Asp	Ala	Arg	Gln	Phe	Ser	Lys	His	Val	Gly	Arg	225	230	235	240
Ser	Gln	Phe	Ser	Val	Ile	Arg	Asp	Ala	Gly	His	Phe	Leu	Asp	Met	Glu	245	250	255	
Asn	Lys	Thr	Ala	Cys	Glu	Asn	Thr	Arg	Asn	Val	Met	Leu	Gly	Phe	Leu	260	265	270	
Lys	Pro	Thr	Val	Arg	Glu	Pro	Arg	Gln	Arg	Tyr	Gln	Pro	Val	Gln	Gln	275	280	285	
Gly	Gln	His	Ala	Phe	Ala	Ile	Gly	Ser	Met	Ser	Asn	Lys	Asn	Asn	Asp	290	295	300	
Glu	Leu	Gln	Arg	Gln	Ala	Ser	Glu	Asn	Thr	Leu	Gly	Leu	Asn	Pro	Val	305	310	315	320

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Ile Gly Ile Arg Arg Lys Asp Leu Leu Ser Ser Ala Arg Thr Val Leu	325	330	335	
Arg Gln Ala Val Arg Gln Pro Leu His Ser Ala Lys His Val Ala His	340	345	350	
Phe Gly Leu Glu Leu Lys Asn Val Leu Leu Gly Lys Ser Ser Leu Ala	355	360	365	
Pro Glu Ser Asp Asp Arg Arg Phe Asn Asp Pro Ala Trp Ser Asn Asn	370	375	380	
Pro Leu Tyr Arg Arg Tyr Leu Gln Thr Tyr Leu Ala Trp Arg Lys Glu	385	390	395	400
Leu Gln Asp Trp Ile Gly Asn Ser Asp Leu Ser Pro Gln Asp Ile Ser	405	410	415	
Arg Gly Gln Phe Val Ile Asn Leu Met Thr Glu Ala Met Ala Pro Thr	420	425	430	
Asn Thr Leu Ser Asn Pro Ala Ala Val Lys Arg Phe Phe Glu Thr Gly	435	440	445	
Gly Lys Ser Leu Leu Asp Gly Leu Ser Asn Leu Ala Lys Asp Leu Val	450	455	460	
Asn Asn Gly Gly Met Pro Ser Gln Val Asn Met Asp Ala Phe Glu Val	465	470	475	480
Gly Lys Asn Leu Gly Thr Ser Glu Gly Ala Val Val Tyr Arg Asn Asp	485	490	495	
Val Leu Glu Leu Ile Gln Tyr Lys Pro Ile Thr Glu Gln Val His Ala	500	505	510	
Arg Pro Leu Leu Val Val Pro Pro Gln Ile Asn Lys Phe Tyr Val Phe	515	520	525	
Asp Leu Ser Pro Glu Lys Ser Leu Ala Arg Tyr Cys Leu Arg Ser Gln	530	535	540	
Gln Gln Thr Phe Ile Ile Ser Trp Arg Asn Pro Thr Lys Ala Gln Arg	545	550	555	560
Glu Trp Gly Leu Ser Thr Tyr Ile Asp Ala Leu Lys Glu Ala Val Asp	565	570	575	

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Ala Val Leu Ala Ile Thr Gly Ser Lys Asp Leu Asn Met Leu Gly Ala	580	585	590
Cys Ser Gly Gly Ile Thr Cys Thr Ala Leu Val Gly His Tyr Ala Ala	595	600	605
Leu Gly Glu Asn Lys Val Asn Ala Leu Thr Leu Leu Val Ser Val Leu	610	615	620
Asp Thr Thr Met Asp Asn Gln Val Ala Leu Phe Val Asp Glu Gln Thr	625	630	635
Leu Glu Ala Ala Lys Arg His Ser Tyr Gln Ala Gly Val Leu Glu Gly	645	650	655
Ser Glu Met Ala Lys Val Phe Ala Trp Met Arg Pro Asn Asp Leu Ile	660	665	670
Trp Asn Tyr Trp Val Asn Asn Tyr Leu Leu Gly Asn Glu Pro Pro Val	675	680	685
Phe Asp Ile Leu Phe Trp Asn Asn Asp Thr Thr Arg Leu Pro Ala Ala	690	695	700
Phe His Gly Asp Leu Ile Glu Met Phe Lys Ser Asn Pro Leu Thr Arg	705	710	715
Pro Asp Ala Leu Glu Val Cys Gly Thr Pro Ile Asp Leu Lys Gln Val	725	730	735
Lys Cys Asp Ile Tyr Ser Leu Ala Gly Thr Asn Asp His Ile Thr Pro	740	745	750
Trp Gln Ser Cys Tyr Arg Ser Ala His Leu Phe Gly Gly Lys Ile Glu	755	760	765
Phe Val Leu Ser Asn Ser Gly His Ile Gln Ser Ile Leu Asn Pro Pro	770	775	780
Gly Asn Pro Lys Ala Arg Phe Met Thr Gly Ala Asp Arg Pro Gly Asp	785	790	795
Pro Val Ala Trp Gln Glu Asn Ala Thr Lys His Ala Asp Ser Trp Trp	805	810	815
Leu His Trp Gln Ser Trp Leu Gly Glu Arg Ala Gly Glu Leu Glu Lys	820	825	830

Ala Pro Thr Arg Leu Gly Asn Arg Ala Tyr Ala Ala Gly Glu Ala Ser
835 840 845

Pro Gly Thr Tyr Val His Glu Arg
850 855

<210> 36
<211> 1731
<212> DNA
<213> Zoogloea ramigera

<220>
<221> gene
<222> (1)..(1731)
<223> phbC gene

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atgttgcagg atatcggcgt tgcgctcaaa ccggaagcga tggagcagct gaaaaacgat 180
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ttcctgaccc agcatggcgg caagaaggtc aagcccaagg ccaagcccgg caacgcccgc 1680
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650E2D " 2494950

<210> 37
 <211> 576
 <212> PRT
 <213> Zoogloea ramigera

<220>
 <221> PEPTIDE
 <222> (1)..(576)
 <223> synthase

<400> 37
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 Thr Glu Ala Asn Pro Met Ala Thr Met Leu Gln Asp Ile Gly Val Ala
 35 40 45
 Leu Lys Pro Glu Ala Met Glu Gln Leu Lys Asn Asp Tyr Leu Arg Asp
 50 55 60
 Phe Thr Ala Leu Trp Gln Asp Phe Leu Ala Gly Lys Ala Pro Ala Val
 65 70 75 80
 Gln Arg Pro Arg Phe Ser Ser Ala Ala Trp Gln Gly Asn Pro Met Ser
 85 90 95
 Ala Phe Asn Ala Ala Ser Tyr Leu Leu Asn Ala Lys Phe Leu Ser Ala
 100 105 110
 Met Val Glu Ala Val Asp Thr Ala Pro Gln Gln Lys Gln Lys Ile Arg
 115 120 125
 Phe Ala Val Gln Gln Val Ile Asp Ala Met Ser Pro Ala Asn Phe Leu
 130 135 140
 Ala Thr Asn Pro Glu Ala Gln Gln Lys Leu Ile Glu Thr Lys Gly Glu
 145 150 155 160
 Ser Leu Thr Arg Gly Leu Val Asn Met Leu Gly Asp Ile Asn Met Leu
 165 170 175
 Gly Asp Ile Asn Asn Gly His Ile Ser Leu Ser Asp Glu Ser Ala Phe
 180 185 190
 Glu Val Gly Arg Asn Leu Ala Ile Thr Pro Gly Thr Val Ile Tyr Glu

650E2D"2493E5D

660E20" 24B49E60

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210	215	220
Ser Gln Arg Pro Leu Leu Met Val Pro Pro Cys Ile Asn Lys Phe Tyr		
225	230	235
Ile Leu Asp Leu Gln Pro Glu Asn Ser Leu Val Arg Tyr Ala Val Glu		
245	250	255
Gln Gly Asn Thr Val Phe Leu Ile Ser Trp Ser Asn Pro Asp Lys Ser		
260	265	270
Leu Ala Gly Thr Thr Trp Asp Asp Tyr Val Glu Gln Gly Val Ile Glu		
275	280	285
Ala Ile Arg Ile Val Gln Asp Val Ser Gly Gln Asp Lys Leu Asn Met		
290	295	300
Phe Gly Phe Cys Val Gly Gly Thr Ile Val Ala Thr Ala Leu Ala Val		
305	310	315
Leu Ala Ala Arg Gly Gln His Pro Ala Ala Ser Leu Thr Leu Leu Thr		
325	330	335
Thr Phe Leu Asp Phe Ser Asp Thr Gly Cys Ser Thr Ser Cys Arg Glu		
340	345	350
Thr Gln Val Ala Leu Arg Glu Gln Gln Leu Arg Asp Gly Gly Leu Met		
355	360	365
Pro Gly Arg Asp Leu Ala Ser Thr Phe Ser Ser Leu Arg Pro Asn Asp		
370	375	380
Leu Val Trp Asn Tyr Val Gln Ser Asn Tyr Leu Lys Gly Asn Glu Pro		
385	390	395
Ala Ala Phe Asp Leu Leu Phe Trp Asn Ser Asp Ser Thr Asn Leu Pro		
405	410	415
Gly Pro Met Phe Cys Trp Tyr Leu Arg Asn Thr Tyr Leu Glu Asn Ser		
420	425	430
Leu Lys Val Pro Gly Lys Leu Thr Val Ala Gly Glu Lys Ile Asp Leu		
435	440	445
Gly Leu Ile Asp Ala Pro Ala Phe Ile Tyr Gly Ser Arg Glu Asp His		

450

455

460

Ile Val Pro Trp Met Ser Ala Tyr Gly Ser Leu Asp Ile Leu Asn Gln
465 470 475 480

Gly Lys Pro Gly Ala Asn Arg Phe Val Leu Gly Ala Ser Gly His Ile
485 490 495

Ala Gly Val Ile Asn Ser Val Ala Lys Asn Lys Arg Thr Tyr Trp Ile
500 505 510

Asn Asp Gly Gly Ala Ala Asp Ala Gln Ala Trp Phe Asp Gly Ala Gln
515 520 525

Glu Val Pro Gly Ser Trp Trp Pro Gln Trp Ala Gly Phe Leu Thr Gln
530 535 540

His Gly Gly Lys Lys Val Lys Pro Lys Ala Lys Pro Gly Asn Ala Arg
545 550 555 560

Tyr Thr Ala Ile Glu Ala Ala Pro Gly Arg Tyr Val Lys Ala Lys Gly
565 570 575

<210> 38

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide primer- C5 up I

<400> 38

ggagctcagg aggttttatg agtaacaaga acaacgatga gc

42

<210> 39

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide primer-C5 up II

<400> 39
cgggatccgc ccttggttt gacgtaacgg

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<210> 40
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer- C5 dw I

<400> 40
cgggatccag taacaagaac aacgatgagc

30

<210> 41
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer- C5 dw II

<400> 41
gctctagaag ctttcagccc ttggctttga cgtaacgg

38

<210> 42
<211> 405
<212> DNA
<213> Aeromonas caviae

<220>
<221> gene
<222> (1)..(405)
<223> phbJ gene

<400> 42
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gccttcgccg ccaccacggc gttcgagcgg cccatagtc acggcatgct gctcgccagc 180
ctcttctccg ggctgctggg ccagcagttg ccgggcaagg ggagcatcta tctgggtcaa 240
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accgcccttc gcgaggacaa gcccatcgcc accctgacca cccgcattct caccacaggc 360
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<210> 43
<211> 134

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[illegible]

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[illegible]

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[illegible][illegible][illegible][illegible][illegible]

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00000000000000000000000000000000

<400> 44

cgggatccag cgcacaatcc ctggaagtag

30

<210> 45

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

oligonucleotide primer-J12 dw II

<400> 45

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38

<210> 46

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: J12 up I

<400> 46

aggagctcag gaggttttat gagcgacaa tccctggaag tag

43

<210> 47

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

oligonucleotide primer- J12 up II

<400> 47

cgggatccag gcagcttgac cacggcttcc

30

<210> 48

<211> 2139

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zoogloea
ramigera and Aeromonas caviae phaC-linker-phbJ
fusion gene

<220>
 <221> gene
 <222> (1) .. (2139)

<400> 48

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atgttgcagg atatcggcgt tgcgctcaaa ccggaagcga tggagcagct gaaaaacgat 180
tatctgcgtg acttcaccgc gttgtggcag gatttttttg ctggcaaggc gccagccgtc 240
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<210> 49
 <211> 712
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthase (R)
specific enoyl-CoA transferase Fusion Protein

<220>

<221> PEPTIDE

<222> (1)..(712)

<400> 49

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Thr Glu Ala Asn Pro Met Ala Thr Met Leu Gln Asp Ile Gly Val Ala
35 40 45

Leu Lys Pro Glu Ala Met Glu Gln Leu Lys Asn Asp Tyr Leu Arg Asp
50 55 60

Phe Thr Ala Leu Trp Gln Asp Phe Leu Ala Gly Lys Ala Pro Ala Val
65 70 75 80

Gln Arg Pro Arg Phe Ser Ser Ala Ala Trp Gln Gly Asn Pro Met Ser
85 90 95

Ala Phe Asn Ala Ala Ser Tyr Leu Leu Asn Ala Lys Phe Leu Ser Ala
100 105 110

Met Val Glu Ala Val Asp Thr Ala Pro Gln Gln Lys Gln Lys Ile Arg
115 120 125

Phe Ala Val Gln Gln Val Ile Asp Ala Met Ser Pro Ala Asn Phe Leu
130 135 140

Ala Thr Asn Pro Glu Ala Gln Gln Lys Leu Ile Glu Thr Lys Gly Glu
145 150 155 160

Ser Leu Thr Arg Gly Leu Val Asn Met Leu Gly Asp Ile Asn Met Leu
165 170 175

Gly Asp Ile Asn Asn Gly His Ile Ser Leu Ser Asp Glu Ser Ala Phe
180 185 190

Glu Val Gly Arg Asn Leu Ala Ile Thr Pro Gly Thr Val Ile Tyr Glu
195 200 205

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Asn	Pro	Leu	Phe	Gln	Leu	Ile	Gln	Tyr	Thr	Pro	Thr	Thr	Pro	Thr	Val	210	215	220	
Ser	Gln	Arg	Pro	Leu	Leu	Met	Val	Pro	Pro	Cys	Ile	Asn	Lys	Phe	Tyr	225	230	235	240
Ile	Leu	Asp	Leu	Gln	Pro	Glu	Asn	Ser	Leu	Val	Arg	Tyr	Ala	Val	Glu	245	250	255	
Gln	Gly	Asn	Thr	Val	Phe	Leu	Ile	Ser	Trp	Ser	Asn	Pro	Asp	Lys	Ser	260	265	270	
Leu	Ala	Gly	Thr	Thr	Trp	Asp	Asp	Tyr	Val	Glu	Gln	Gly	Val	Ile	Glu	275	280	285	
Ala	Ile	Arg	Ile	Val	Gln	Asp	Val	Ser	Gly	Gln	Asp	Lys	Leu	Asn	Met	290	295	300	
Phe	Gly	Phe	Cys	Val	Gly	Gly	Thr	Ile	Val	Ala	Thr	Ala	Leu	Ala	Val	305	310	315	320
Leu	Ala	Ala	Arg	Gly	Gln	His	Pro	Ala	Ala	Ser	Leu	Thr	Leu	Leu	Thr	325	330	335	
Thr	Phe	Leu	Asp	Phe	Ser	Asp	Thr	Gly	Cys	Ser	Thr	Ser	Cys	Arg	Glu	340	345	350	
Thr	Gln	Val	Ala	Leu	Arg	Glu	Gln	Gln	Leu	Arg	Asp	Gly	Gly	Leu	Met	355	360	365	
Pro	Gly	Arg	Asp	Leu	Ala	Ser	Thr	Phe	Ser	Ser	Leu	Arg	Pro	Asn	Asp	370	375	380	
Leu	Val	Trp	Asn	Tyr	Val	Gln	Ser	Asn	Tyr	Leu	Lys	Gly	Asn	Glu	Pro	385	390	395	400
Ala	Ala	Phe	Asp	Leu	Leu	Phe	Trp	Asn	Ser	Asp	Ser	Thr	Asn	Leu	Pro	405	410	415	
Gly	Pro	Met	Phe	Cys	Trp	Tyr	Leu	Arg	Asn	Thr	Tyr	Leu	Glu	Asn	Ser	420	425	430	
Leu	Lys	Val	Pro	Gly	Lys	Leu	Thr	Val	Ala	Gly	Glu	Lys	Ile	Asp	Leu	435	440	445	
Gly	Leu	Ile	Asp	Ala	Pro	Ala	Phe	Ile	Tyr	Gly	Ser	Arg	Glu	Asp	His	450	455	460	

660620-2484966

Ile Val Pro Trp Met Ser Ala Tyr Gly Ser Leu Asp Ile Leu Asn Gln			
465	470	475	480
Gly Lys Pro Gly Ala Asn Arg Phe Val Leu Gly Ala Ser Gly His Ile			
	485	490	495
Ala Gly Val Ile Asn Ser Val Ala Lys Asn Lys Arg Thr Tyr Trp Ile			
	500	505	510
Asn Asp Gly Gly Ala Ala Asp Ala Gln Ala Trp Phe Asp Gly Ala Gln			
	515	520	525
Glu Val Pro Gly Ser Trp Trp Pro Gln Trp Ala Gly Phe Leu Thr Gln			
	530	535	540
His Gly Gly Lys Lys Val Lys Pro Lys Ala Lys Pro Gly Asn Ala Arg			
545	550	555	560
Tyr Thr Ala Ile Glu Ala Ala Pro Gly Arg Tyr Val Lys Ala Lys Gly			
	565	570	575
Gly Ser Met Ser Ala Gln Ser Leu Glu Val Gly Gln Lys Ala Arg Leu			
	580	585	590
Ser Lys Arg Phe Gly Ala Ala Glu Val Ala Ala Phe Ala Ala Leu Ser			
	595	600	605
Glu Asp Phe Asn Pro Leu His Leu Asp Pro Ala Phe Ala Ala Thr Thr			
	610	615	620
Ala Phe Glu Arg Pro Ile Val His Gly Met Leu Leu Ala Ser Leu Phe			
625	630	635	640
Ser Gly Leu Leu Gly Gln Gln Leu Pro Gly Lys Gly Ser Ile Tyr Leu			
	645	650	655
Gly Gln Ser Leu Ser Phe Lys Leu Pro Val Phe Val Gly Asp Glu Val			
	660	665	670
Thr Ala Glu Val Glu Val Thr Ala Leu Arg Glu Asp Lys Pro Ile Ala			
	675	680	685
Thr Leu Thr Thr Arg Ile Phe Thr Gln Gly Gly Ala Leu Ala Val Thr			
	690	695	700
Gly Glu Ala Val Val Lys Leu Pro			
705	710		

<210> 50
 <211> 2139
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: *Aeromonas*
caviae and *Zoogloea ramigera* phbJ-linker-phaC
 fusion gene

<220>

<221> gene

<222> (1)..(2139)

<400> 50

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650520"249364947"073099

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<210> 51

<211> 712

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: (R) - specific
 enoyl-CoA transferase Synthase Fusion Protein

<220>

<221> PEPTIDE

<222> (1)..(712)

<400> 51

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Arg	Phe	Gly	Ala	Ala	Glu	Val	Ala	Ala	Phe	Ala	Ala	Leu	Ser	Glu	Asp	20	25	30	
Phe	Asn	Pro	Leu	His	Leu	Asp	Pro	Ala	Phe	Ala	Ala	Thr	Thr	Ala	Phe	35	40	45	
Glu	Arg	Pro	Ile	Val	His	Gly	Met	Leu	Leu	Ala	Ser	Leu	Phe	Ser	Gly	50	55	60	
Leu	Leu	Gly	Gln	Gln	Leu	Pro	Gly	Lys	Gly	Ser	Ile	Tyr	Leu	Gly	Gln	65	70	75	80
Ser	Leu	Ser	Phe	Lys	Leu	Pro	Val	Phe	Val	Gly	Asp	Glu	Val	Thr	Ala	85	90	95	
Glu	Val	Glu	Val	Thr	Ala	Leu	Arg	Glu	Asp	Lys	Pro	Ile	Ala	Thr	Leu	100	105	110	
Thr	Thr	Arg	Ile	Phe	Thr	Gln	Gly	Gly	Ala	Leu	Ala	Val	Thr	Gly	Glu	115	120	125	
Ala	Val	Val	Lys	Leu	Pro	Gly	Ser	Met	Asn	Leu	Pro	Asp	Pro	Gln	Ala	130	135	140	
Ile	Ala	Asn	Ala	Trp	Met	Ser	Gln	Val	Gly	Asp	Pro	Ser	Gln	Trp	Gln	145	150	155	160

003649560 241349560

Ser Trp Phe Ser Lys Ala Pro Thr Thr Glu Ala Asn Pro Met Ala Thr	165	170	175	
Met Leu Gln Asp Ile Gly Val Ala Leu Lys Pro Glu Ala Met Glu Gln	180	185	190	
Leu Lys Asn Asp Tyr Leu Arg Asp Phe Thr Ala Leu Trp Gln Asp Phe	195	200	205	
Leu Ala Gly Lys Ala Pro Ala Val Gln Arg Pro Arg Phe Ser Ser Ala	210	215	220	
Ala Trp Gln Gly Asn Pro Met Ser Ala Phe Asn Ala Ala Ser Tyr Leu	225	230	235	240
Leu Asn Ala Lys Phe Leu Ser Ala Met Val Glu Ala Val Asp Thr Ala	245	250	255	
Pro Gln Gln Lys Gln Lys Ile Arg Phe Ala Val Gln Gln Val Ile Asp	260	265	270	
Ala Met Ser Pro Ala Asn Phe Leu Ala Thr Asn Pro Glu Ala Gln Gln	275	280	285	
Lys Leu Ile Glu Thr Lys Gly Glu Ser Leu Thr Arg Gly Leu Val Asn	290	295	300	
Met Leu Gly Asp Ile Asn Met Leu Gly Asp Ile Asn Asn Gly His Ile	305	310	315	320
Ser Leu Ser Asp Glu Ser Ala Phe Glu Val Gly Arg Asn Leu Ala Ile	325	330	335	
Thr Pro Gly Thr Val Ile Tyr Glu Asn Pro Leu Phe Gln Leu Ile Gln	340	345	350	
Tyr Thr Pro Thr Thr Pro Thr Val Ser Gln Arg Pro Leu Leu Met Val	355	360	365	
Pro Pro Cys Ile Asn Lys Phe Tyr Ile Leu Asp Leu Gln Pro Glu Asn	370	375	380	
Ser Leu Val Arg Tyr Ala Val Glu Gln Gly Asn Thr Val Phe Leu Ile	385	390	395	400
Ser Trp Ser Asn Pro Asp Lys Ser Leu Ala Gly Thr Thr Trp Asp Asp	405	410	415	

Tyr	Val	Glu	Gln	Gly	Val	Ile	Glu	Ala	Ile	Arg	Ile	Val	Gln	Asp	Val	420	425	430
Ser	Gly	Gln	Asp	Lys	Leu	Asn	Met	Phe	Gly	Phe	Cys	Val	Gly	Gly	Thr	435	440	445
Ile	Val	Ala	Thr	Ala	Leu	Ala	Val	Leu	Ala	Ala	Arg	Gly	Gln	His	Pro	450	455	460
Ala	Ala	Ser	Leu	Thr	Leu	Leu	Thr	Thr	Phe	Leu	Asp	Phe	Ser	Asp	Thr	465	470	475
Gly	Cys	Ser	Thr	Ser	Cys	Arg	Glu	Thr	Gln	Val	Ala	Leu	Arg	Glu	Gln	485	490	495
Gln	Leu	Arg	Asp	Gly	Gly	Leu	Met	Pro	Gly	Arg	Asp	Leu	Ala	Ser	Thr	500	505	510
Phe	Ser	Ser	Leu	Arg	Pro	Asn	Asp	Leu	Val	Trp	Asn	Tyr	Val	Gln	Ser	515	520	525
Asn	Tyr	Leu	Lys	Gly	Asn	Glu	Pro	Ala	Ala	Phe	Asp	Leu	Leu	Phe	Trp	530	535	540
Asn	Ser	Asp	Ser	Thr	Asn	Leu	Pro	Gly	Pro	Met	Phe	Cys	Trp	Tyr	Leu	545	550	555
Arg	Asn	Thr	Tyr	Leu	Glu	Asn	Ser	Leu	Lys	Val	Pro	Gly	Lys	Leu	Thr	565	570	575
Val	Ala	Gly	Glu	Lys	Ile	Asp	Leu	Gly	Leu	Ile	Asp	Ala	Pro	Ala	Phe	580	585	590
Ile	Tyr	Gly	Ser	Arg	Glu	Asp	His	Ile	Val	Pro	Trp	Met	Ser	Ala	Tyr	595	600	605
Gly	Ser	Leu	Asp	Ile	Leu	Asn	Gln	Gly	Lys	Pro	Gly	Ala	Asn	Arg	Phe	610	615	620
Val	Leu	Gly	Ala	Ser	Gly	His	Ile	Ala	Gly	Val	Ile	Asn	Ser	Val	Ala	625	630	635
Lys	Asn	Lys	Arg	Thr	Tyr	Trp	Ile	Asn	Asp	Gly	Gly	Ala	Ala	Asp	Ala	645	650	655
Gln	Ala	Trp	Phe	Asp	Gly	Ala	Gln	Glu	Val	Pro	Gly	Ser	Trp	Trp	Pro	660	665	670

Gln Trp Ala Gly Phe Leu Thr Gln His Gly Gly Lys Lys Val Lys Pro
 675 680 685

Lys Ala Lys Pro Gly Asn Ala Arg Tyr Thr Ala Ile Glu Ala Ala Pro
 690 695 700

Gly Arg Tyr Val Lys Ala Lys Gly
 705 710

<210> 52
 <211> 1185
 <212> DNA
 <213> *Aeromonas caviae*

<220>
 <221> gene
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 <223> bktB gene

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<210> 53
 <211> 394
 <212> PRT
 <213> Artificial Sequence

66062071849560

<220>

<223> Description of Artificial Sequence: thiolase II

<220>

<221> PEPTIDE

<222> (1) .. (394)

<400> 53

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Thr Phe Gly Gly Ser Leu Lys Asp Val Ala Pro Ala Glu Leu Gly Ala
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Leu Val Val Arg Glu Ala Leu Ala Arg Ala Gln Val Ser Gly Asp Asp
35 40 45

Val Gly His Val Val Phe Gly Asn Val Ile Gln Thr Glu Pro Arg Asp
50 55 60

Met Tyr Leu Gly Arg Val Ala Ala Val Asn Gly Gly Val Thr Ile Asn
65 70 75 80

Ala Pro Ala Leu Thr Val Asn Arg Leu Cys Gly Ser Gly Leu Gln Ala
85 90 95

Ile Val Ser Ala Ala Gln Thr Ile Leu Leu Gly Asp Thr Asp Val Ala
100 105 110

Ile Gly Gly Gly Ala Glu Ser Met Ser Arg Ala Pro Tyr Leu Ala Pro
115 120 125

Ala Ala Arg Trp Gly Ala Arg Met Gly Asp Ala Gly Leu Val Asp Met
130 135 140

Met Leu Gly Ala Leu His Asp Pro Phe His Arg Ile His Met Gly Val
145 150 155 160

Thr Ala Glu Asn Val Ala Lys Glu Tyr Asp Ile Ser Arg Ala Gln Gln
165 170 175

Asp Glu Ala Ala Leu Glu Ser His Arg Arg Ala Ser Ala Ala Ile Lys
180 185 190

Ala Gly Tyr Phe Lys Asp Gln Ile Val Pro Val Val Ser Lys Gly Arg
195 200 205

Lys Gly Asp Val Thr Phe Asp Thr Asp Glu His Val Arg His Asp Ala

650520 21349560

660E20" 21849E60

210	215	220
Thr Ile Asp Asp Met Thr Lys Leu Arg Pro Val Phe Val Lys Glu Asn		
225	230	235 240
Gly Thr Val Thr Ala Gly Asn Ala Ser Gly Leu Asn Asp Ala Ala Ala		
245	250	255
Ala Val Val Met Met Glu Arg Ala Glu Ala Glu Arg Arg Gly Leu Lys		
260	265	270
Pro Leu Ala Arg Leu Val Ser Tyr Gly His Ala Gly Val Asp Pro Lys		
275	280	285
Ala Met Gly Ile Gly Pro Val Pro Ala Thr Lys Ile Ala Leu Glu Arg		
290	295	300
Ala Gly Leu Gln Val Ser Asp Leu Asp Val Ile Glu Ala Asn Glu Ala		
305	310	315 320
Phe Ala Ala Gln Ala Cys Ala Val Thr Lys Ala Leu Gly Leu Asp Pro		
325	330	335
Ala Lys Val Asn Pro Asn Gly Ser Gly Ile Ser Leu Gly His Pro Ile		
340	345	350
Gly Ala Thr Gly Ala Leu Ile Thr Val Lys Ala Leu His Glu Leu Asn		
355	360	365
Arg Val Gln Gly Arg Tyr Ala Leu Val Thr Met Cys Ile Gly Gly Gly		
370	375	380
Gln Gly Ile Ala Ala Ile Phe Glu Arg Ile		
385	390	

<210> 54
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
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<400> 54
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<210> 55
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer- A1-II up II

<400> 55
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29

<210> 56
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer- A1-II dw I

<400> 56
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31

<210> 57
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide primer- A1-II dw II

<400> 57
gctctagaag ctttcagata cgctcgaaga tggcggc

37

<210> 58
<211> 1929
<212> DNA
<213> *Ralstonia eutropha*

<220>
<221> gene
<222> (1)..(1929)
<223> bktB-linker-phbB fusion gene

<400> 58
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<210> 59
 <211> 642
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Thiolase II
 Reductase Fusion Protein

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 Thr Phe Gly Gly Ser Leu Lys Asp Val Ala Pro Ala Glu Leu Gly Ala
 20 25 30

Leu Val Val Arg Glu Ala Leu Ala Arg Ala Gln Val Ser Gly Asp Asp
 35 40 45
 Val Gly His Val Val Phe Gly Asn Val Ile Gln Thr Glu Pro Arg Asp
 50 55 60
 Met Tyr Leu Gly Arg Val Ala Ala Val Asn Gly Gly Val Thr Ile Asn
 65 70 75 80
 Ala Pro Ala Leu Thr Val Asn Arg Leu Cys Gly Ser Gly Leu Gln Ala
 85 90 95
 Ile Val Ser Ala Ala Gln Thr Ile Leu Leu Gly Asp Thr Asp Val Ala
 100 105 110
 Ile Gly Gly Gly Ala Glu Ser Met Ser Arg Ala Pro Tyr Leu Ala Pro
 115 120 125
 Ala Ala Arg Trp Gly Ala Arg Met Gly Asp Ala Gly Leu Val Asp Met
 130 135 140
 Met Leu Gly Ala Leu His Asp Pro Phe His Arg Ile His Met Gly Val
 145 150 155 160
 Thr Ala Glu Asn Val Ala Lys Glu Tyr Asp Ile Ser Arg Ala Gln Gln
 165 170 175
 Asp Glu Ala Ala Leu Glu Ser His Arg Arg Ala Ser Ala Ala Ile Lys
 180 185 190
 Ala Gly Tyr Phe Lys Asp Gln Ile Val Pro Val Val Ser Lys Gly Arg
 195 200 205
 Lys Gly Asp Val Thr Phe Asp Thr Asp Glu His Val Arg His Asp Ala
 210 215 220
 Thr Ile Asp Asp Met Thr Lys Leu Arg Pro Val Phe Val Lys Glu Asn
 225 230 235 240
 Gly Thr Val Thr Ala Gly Asn Ala Ser Gly Leu Asn Asp Ala Ala Ala
 245 250 255
 Ala Val Val Met Met Glu Arg Ala Glu Ala Glu Arg Arg Gly Leu Lys
 260 265 270
 Pro Leu Ala Arg Leu Val Ser Tyr Gly His Ala Gly Val Asp Pro Lys
 275 280 285

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00364847-033099

Ala Met Gly Ile Gly Pro Val Pro Ala Thr Lys Ile Ala Leu Glu Arg		
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Ala Gly Leu Gln Val Ser Asp Leu Asp Val Ile Glu Ala Asn Glu Ala		
305	310	315 320
Phe Ala Ala Gln Ala Cys Ala Val Thr Lys Ala Leu Gly Leu Asp Pro		
325	330	335
Ala Lys Val Asn Pro Asn Gly Ser Gly Ile Ser Leu Gly His Pro Ile		
340	345	350
Gly Ala Thr Gly Ala Leu Ile Thr Val Lys Ala Leu His Glu Leu Asn		
355	360	365
Arg Val Gln Gly Arg Tyr Ala Leu Val Thr Met Cys Ile Gly Gly Gly		
370	375	380
Gln Gly Ile Ala Ala Ile Phe Glu Arg Ile Gly Ser Met Thr Gln Arg		
385	390	395 400
Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly Thr Ala Ile Cys		
405	410	415
Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala Gly Cys Gly Pro		
420	425	430
Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln Lys Ala Leu Gly		
435	440	445
Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp Trp Asp Ser Thr		
450	455	460
Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly Glu Val Asp Val		
465	470	475 480
Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val Phe Arg Lys Met		
485	490	495
Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn Leu Thr Ser Leu		
500	505	510
Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala Asp Arg Gly Trp		
515	520	525
Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln Lys Gly Gln Phe		
530	535	540

Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu His Gly Phe Thr
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Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val Thr Val Asn Thr
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Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys Ala Ile Arg Gln
580 585 590

Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val Lys Arg Leu Gly
595 600 605

Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu Ser Ser Glu Glu
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Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn Gly Gly Leu His
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Met Gly

<210> 60

<211> 1929

<212> DNA

<213> *Ralstonia eutropha*

<220>

<221> gene

<222> (1)..(1929)

<223> phbB-linker-bktB fusion gene

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<210> 61

<211> 642

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Reductase
Thiolase II Fusion Protein

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<221> PEPTIDE

<222> (1)..(642)

<400> 61

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Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
      20             25             30

Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
      35             40             45

Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
      50             55             60

Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
      65             70             75             80

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Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val
 85 90 95
 Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn
 100 105 110
 Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
 115 120 125
 Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
 130 135 140
 Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
 145 150 155 160
 His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
 165 170 175
 Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys
 180 185 190
 Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val
 195 200 205
 Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu
 210 215 220
 Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn
 225 230 235 240
 Gly Gly Leu His Met Gly Gly Ser Met Thr Arg Glu Val Val Val Val
 245 250 255
 Ser Gly Val Arg Thr Ala Ile Gly Thr Phe Gly Gly Ser Leu Lys Asp
 260 265 270
 Val Ala Pro Ala Glu Leu Gly Ala Leu Val Val Arg Glu Ala Leu Ala
 275 280 285
 Arg Ala Gln Val Ser Gly Asp Asp Val Gly His Val Val Phe Gly Asn
 290 295 300
 Val Ile Gln Thr Glu Pro Arg Asp Met Tyr Leu Gly Arg Val Ala Ala
 305 310 315 320
 Val Asn Gly Gly Val Thr Ile Asn Ala Pro Ala Leu Thr Val Asn Arg
 325 330 335

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660E20 24849E60

Leu Cys Gly Ser Gly Leu Gln Ala Ile Val Ser Ala Ala Gln Thr Ile	340	345	350
Leu Leu Gly Asp Thr Asp Val Ala Ile Gly Gly Gly Ala Glu Ser Met	355	360	365
Ser Arg Ala Pro Tyr Leu Ala Pro Ala Ala Arg Trp Gly Ala Arg Met	370	375	380
Gly Asp Ala Gly Leu Val Asp Met Met Leu Gly Ala Leu His Asp Pro	385	390	395
Phe His Arg Ile His Met Gly Val Thr Ala Glu Asn Val Ala Lys Glu	405	410	415
Tyr Asp Ile Ser Arg Ala Gln Gln Asp Glu Ala Ala Leu Glu Ser His	420	425	430
Arg Arg Ala Ser Ala Ala Ile Lys Ala Gly Tyr Phe Lys Asp Gln Ile	435	440	445
Val Pro Val Val Ser Lys Gly Arg Lys Gly Asp Val Thr Phe Asp Thr	450	455	460
Asp Glu His Val Arg His Asp Ala Thr Ile Asp Asp Met Thr Lys Leu	465	470	475
Arg Pro Val Phe Val Lys Glu Asn Gly Thr Val Thr Ala Gly Asn Ala	485	490	495
Ser Gly Leu Asn Asp Ala Ala Ala Ala Val Val Met Met Glu Arg Ala	500	505	510
Glu Ala Glu Arg Arg Gly Leu Lys Pro Leu Ala Arg Leu Val Ser Tyr	515	520	525
Gly His Ala Gly Val Asp Pro Lys Ala Met Gly Ile Gly Pro Val Pro	530	535	540
Ala Thr Lys Ile Ala Leu Glu Arg Ala Gly Leu Gln Val Ser Asp Leu	545	550	555
Asp Val Ile Glu Ala Asn Glu Ala Phe Ala Ala Gln Ala Cys Ala Val	565	570	575
Thr Lys Ala Leu Gly Leu Asp Pro Ala Lys Val Asn Pro Asn Gly Ser	580	585	590

Gly Ile Ser Leu Gly His Pro Ile Gly Ala Thr Gly Ala Leu Ile Thr
 595 600 605

Val Lys Ala Leu His Glu Leu Asn Arg Val Gln Gly Arg Tyr Ala Leu
 610 615 620

Val Thr Met Cys Ile Gly Gly Gly Gln Gly Ile Ala Ala Ile Phe Glu
 625 630 635 640

Arg Ile

0936447 073099